

## Abstract of PhD degree works:

Among the world's most important crop plants, barley is ranking the fourth, after maize, rice and wheat in both, in cultivation area and in the production. In the arid and semi arid region, barley has no contestant crop and widely used as human food as well as feed for the farmers' livestock. Genetic diversity is the main sources for crop development and the main tool to overcome the biotic and abiotic threats. Evaluating the genetic diversity gives us a better understanding of conserving and of exploiting the genetic diversity in sustainable manner. Moreover, identifying and verifying the domestication locations and events will enhance our understanding of the genetic diversity within and outside its domestication center(s). Therefore, this project was established to study the barley domestication and its genetic diversity in two highly diverse regions, West Asia and North Africa (WANA) and Horn of Africa.

The introduction of the thesis in addition to the first paper gives an overview about barley in WANA and the Horn of Africa. Our current knowledge about the genetic diversity of wild (*Hordeum vulgare* ssp. *spontaneum*) and cultivated barley (*H. vulgare* ssp. *vulgare*) in WANA and Horn of Africa is also presented. Emphasis is put on the long debate regarding the domestication locations and events of barley. Moreover, the discussion regarding the loss of diversity due to the domestication, due to the dispersal from the domestication center and due to the modern plant breeding is presented.

The experimental work can be divided into three major subjects presented in three papers. The first subject that is presented in the second paper deals with the Horn of Africa as a centre of barley diversification and a potential domestication site. According to a widely accepted theory on barley domestication, wild barley from the Fertile Crescent (FC) is the progenitor of all cultivated barley. To determine whether barley has undergone one or more domestication events, barley accessions from three continents were studied by the nuclear and chloroplast Simple Sequence Repeat (SSR) markers. In addition, the sequence polymorphism in a fragment from the non-coding region of chloroplast DNA was analyzed. A clear separation was found between Eritrean/Ethiopian barley and barley from WANA as well as from Europe. The results clearly indicate that the wild barley as it is found today in the FC might not be the progenitor of the barley cultivated in Eritrea/Ethiopia. Consequently, an independent domestication might have taken place at the Horn of Africa.

The second subject was presented in the third paper entitled "High genetic diversity revealed in barley collected from small-scale farmer's fields in Eritrea". Significant genetic diversity was found within the Eritrean barley fields. Out of 240 spikes collected from 24 fields, only two spikes from geographically distant fields were genetically similar. Individual farmers' fields were found to possess 97.3% of the genetic variation present in the Eritrean barley. In this paper, a strategy to improve the barley yield in Eritrea and to facilitate the *in situ* conservation is discussed.

The last subject was presented in the fourth paper on the "Genetic Diversity and Population Structure of Wild and Cultivated Barley from West Asia and North Africa". Population structure and relationships within and among 185 accessions of wild and cultivated barley from five countries in WANA region were studied. The landraces from different countries of the Near East showed genetic diversity that was nearly as high as the wild barley from the same country. Structure analysis of WANA barley was studied. Wild barley from Palestine represented the group with the highest diversity and the most complex structure. The relationship between cultivated barley and wild barley was discussed. Moreover, the importance of WANA barley was emphasis and discussed together with the conservation and exploitation of its genetic diversity.